

PlantPAN: Plant promoter analysis navigator, for identifying elements with distance constraint in plant gene groups

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Citation Report

#	ARTICLE	IF	CITATIONS
1	cis-Regulatory elements in plant cell signaling. <i>Current Opinion in Plant Biology</i> , 2009, 12, 643-649.	3.5	105
2	The <i>LP2</i> leucine-rich repeat receptor kinase gene promoter directs organ-specific, light-responsive expression in transgenic rice. <i>Plant Biotechnology Journal</i> , 2009, 7, 867-882.	4.1	34
3	Storage products and transcriptional analysis of the endosperm of cultivated wheat and two wild wheat species. <i>Journal of Applied Genetics</i> , 2010, 51, 431-447.	1.0	13
4	The tissue expression pattern of the <i>AtGRP5</i> regulatory region is controlled by a combination of positive and negative elements. <i>Plant Cell Reports</i> , 2010, 29, 461-471.	2.8	8
5	Molecular characterization and functional analysis of Glycine max sterol methyl transferase 2 genes involved in plant membrane sterol biosynthesis. <i>Plant Molecular Biology</i> , 2010, 74, 503-518.	2.0	23
6	Identification and expression analysis of microRNAs and targets in the biofuel crop sugarcane. <i>BMC Plant Biology</i> , 2010, 10, 260.	1.6	76
7	Boron Toxicity Tolerance in Barley through Reduced Expression of the Multifunctional Aquaporin HvNIP2;1 Å. <i>Plant Physiology</i> , 2010, 153, 1706-1715.	2.3	159
8	Isolation and Phylogenetic Footprinting Analysis of the 5' Regulatory Region of the Floral Homeotic Gene <i>OrcPI</i> from <i>Orchis italica</i> (Orchidaceae). <i>Journal of Heredity</i> , 2010, 101, 124-131.	1.0	7
9	Hypoxia-responsive microRNAs and trans-acting small interfering RNAs in Arabidopsis. <i>Journal of Experimental Botany</i> , 2010, 61, 165-177.	2.4	184
10	Constructing gene regulatory networks for long term photosynthetic light acclimation in <i>Arabidopsis thaliana</i> . <i>BMC Bioinformatics</i> , 2011, 12, 335.	1.2	18
11	Toward microRNA-mediated gene regulatory networks in plants. <i>Briefings in Bioinformatics</i> , 2011, 12, 645-659.	3.2	53
12	The NFI-Regulome Database: A tool for annotation and analysis of control regions of genes regulated by Nuclear Factor I transcription factors. <i>Journal of Clinical Bioinformatics</i> , 2011, 1, 4.	1.2	22
13	Hypoxia responsive gene expression is mediated by various subsets of transcription factors and miRNAs that are determined by the actual oxygen availability. <i>New Phytologist</i> , 2011, 190, 442-456.	3.5	149
14	<i>In silico</i> analysis of phytoene synthase and its promoter reveals hints for regulation mechanisms of carotenogenesis in <i>Dunaliella bardawil</i> . <i>Bioinformatics</i> , 2011, 27, 2201-2208.	1.8	25
15	Molecular characterization of a phenylalanine ammonia-lyase gene (<i>BoPAL1</i>) from <i>Bambusa oldhamii</i> . <i>Molecular Biology Reports</i> , 2011, 38, 283-290.	1.0	49
16	Differential transcript abundance and genotypic variation of four putative allergen-encoding gene families in melting peach. <i>Tree Genetics and Genomes</i> , 2011, 7, 903-916.	0.6	20
17	Characterization of the glyoxalase 1 gene <i>TcGLX1</i> in the metal hyperaccumulator plant <i>Thlaspi caerulescens</i> . <i>Planta</i> , 2011, 233, 1173-1184.	1.6	21
18	Comparative transcription profiling analyses of maize reveals candidate defensive genes for seedling resistance against corn earworm. <i>Molecular Genetics and Genomics</i> , 2011, 285, 517-525.	1.0	12

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19	Integration of molecular biology tools for identifying promoters and genes abundantly expressed in flowers of <i>Oncidium Gower Ramsey</i> . <i>BMC Plant Biology</i> , 2011, 11, 60.	1.6	27
20	Isolation and functional characterization of a cotton ubiquitination-related promoter and 5'UTR that drives high levels of expression in root and flower tissues. <i>BMC Biotechnology</i> , 2011, 11, 115.	1.7	18
21	Oxidative DNA Damage Bypass in <i>Arabidopsis thaliana</i> Requires DNA Polymerase Î» and Proliferating Cell Nuclear Antigen 2. <i>Plant Cell</i> , 2011, 23, 806-822.	3.1	47
22	Ntann12 annexin expression is induced by auxin in tobacco roots. <i>Journal of Experimental Botany</i> , 2011, 62, 4055-4065.	2.4	30
23	Evolutionary divergence and limits of conserved non-coding sequence detection in plant genomes. <i>Nucleic Acids Research</i> , 2011, 39, 6029-6043.	6.5	32
24	Novel Insights into Regulation of Asparagine Synthetase in Conifers. <i>Frontiers in Plant Science</i> , 2012, 3, 100.	1.7	50
25	Gibberellins regulate the transcription of the continuous flowering regulator, RoKSN, a rose TFL1 homologue. <i>Journal of Experimental Botany</i> , 2012, 63, 6543-6554.	2.4	61
26	Insight into plant annexin function. <i>Plant Signaling and Behavior</i> , 2012, 7, 524-528.	1.2	35
27	Impaired Auxin Biosynthesis in the defective endosperm18 Mutant Is Due to Mutational Loss of Expression in the <i>ZmYuc1</i> Gene Encoding Endosperm-Specific YUCCA1 Protein in Maize. <i>Plant Physiology</i> , 2012, 160, 1318-1328.	2.3	128
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30	Thousands of Cis-Regulatory Sequence Combinations Are Shared by <i>Arabidopsis</i> and Poplar. <i>Plant Physiology</i> , 2012, 158, 145-155.	2.3	29
31	Functional characterization of two almond C-repeat-binding factors involved in cold response. <i>Tree Physiology</i> , 2012, 32, 1113-1128.	1.4	39
32	The OsGEX2 Gene Promoter Confers Sperm Cell Expression in Transgenic Rice. <i>Plant Molecular Biology Reporter</i> , 2012, 30, 1138-1148.	1.0	17
33	The DNA-binding activity of an AP2 protein is involved in transcriptional regulation of a stress-responsive gene, SiWD40, in foxtail millet. <i>Genomics</i> , 2012, 100, 252-263.	1.3	48
34	Six Regulatory Elements Lying in the Promoter Region Imply the Functional Diversity of Chloroplast GAPDH in <i>Duanliella bardawil</i> . <i>Journal of Agricultural and Food Chemistry</i> , 2012, 60, 9211-9220.	2.4	3
35	Population-genetic analysis of HvABCG31 promoter sequence in wild barley (<i>Hordeum vulgare</i> ssp.)	3.2	11
36	MicroRNA Targets, a new AthaMap web-tool for genome-wide identification of miRNA targets in <i>Arabidopsis thaliana</i> . <i>BioData Mining</i> , 2012, 5, 7.	2.2	23

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37	Expression analysis of calmodulin and calmodulin-like genes from rice, <i>Oryza sativa</i> L.. BMC Research Notes, 2012, 5, 625.	0.6	46
38	The NAC transcription factor gene ANAC072 is differentially expressed in <i>Arabidopsis thaliana</i> in response to microbe-associated molecular pattern (MAMP) molecules. Physiological and Molecular Plant Pathology, 2012, 80, 19-27.	1.3	10
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45	Expression and tissue-specific localization of nitrate-responsive miRNAs in roots of maize seedlings. Plant, Cell and Environment, 2012, 35, 1137-1155.	2.8	64
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47	Genome-wide identification and analysis of microRNA responding to long-term waterlogging in crown roots of maize seedlings. Physiologia Plantarum, 2013, 147, 181-193.	2.6	70
48	Using an ensemble of statistical metrics to quantify large sets of plant transcription factor binding sites. Plant Methods, 2013, 9, 12.	1.9	2
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56	The SIFRK4 promoter is active only during late stages of pollen and anther development. <i>Plant Science</i> , 2013, 199-200, 61-70.	1.7	37
57	CBF gene expression in peach leaf and bark tissues is gated by a circadian clock. <i>Tree Physiology</i> , 2013, 33, 866-877.	1.4	45
58	Elucidating the evolutionary history and expression patterns of nucleoside phosphorylase paralogs (vegetative storage proteins) in <i>Populus</i> and the plant kingdom. <i>BMC Plant Biology</i> , 2013, 13, 118.	1.6	17
59	Expression of the high light-inducible <i>Dunaliella</i> LIP promoter in <i>Chlamydomonas reinhardtii</i> . <i>Planta</i> , 2013, 238, 1147-1156.	1.6	24
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61	Molecular characterization of <i>Quercus suber</i> MYB1, a transcription factor up-regulated in cork tissues. <i>Journal of Plant Physiology</i> , 2013, 170, 172-178.	1.6	31
62	<i>Arabidopsis</i> suppressor mutant of <i>abh1</i> shows a new face of the already known players: ABH1 (CBP80) and ABI4 in response to ABA and abiotic stresses during seed germination. <i>Plant Molecular Biology</i> , 2013, 81, 189-209.	2.0	32
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73	Higher plant transformation: principles and molecular tools. <i>International Journal of Developmental Biology</i> , 2013, 57, 483-494.	0.3	60
74	miRNAs mediate SnRK1-dependent energy signaling in <i>Arabidopsis</i> . <i>Frontiers in Plant Science</i> , 2013, 4, 197.	1.7	64
75	Floral primordia-targeted ACS (1-aminocyclopropane-1-carboxylate synthase) expression in transgenic <i>Cucumis melo</i> implicates fine tuning of ethylene production mediating unisexual flower development. <i>Planta</i> , 2014, 240, 797-808.	1.6	35
76	Comparative analysis of ADS gene promoter in seven <i>Artemisia</i> species. <i>Journal of Genetics</i> , 2014, 93, 767-774.	0.4	1
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80	Conserved cis-regulatory modules in promoters of genes encoding wheat high-molecular-weight glutenin subunits. <i>Frontiers in Plant Science</i> , 2014, 5, 621.	1.7	44
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85	Isolation and Characterization of Three New Promoters from <i>Gossypium hirsutum</i> that Show High Activity in Reproductive Tissues. <i>Plant Molecular Biology Reporter</i> , 2014, 32, 630-643.	1.0	12
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89	Resources for systems biology in rice. <i>Journal of Plant Biology</i> , 2014, 57, 80-92.	0.9	34
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97	Integrating bioinformatic resources to predict transcription factors interacting with cis-sequences conserved in co-regulated genes. BMC Genomics, 2014, 15, 317.	1.2	19
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104	Advantages and disadvantages in usage of bioinformatic programs in promoter region analysis. Proceedings of SPIE, 2015, , .	0.8	1
105	Molecular cloning and characterization of salt inducible dehydrin gene from the C4 plant <i>Pennisetum glaucum</i> . Plant Gene, 2015, 4, 55-63.	1.4	30
106	Genome-wide identification and characterization of the aquaporin gene family in <i>Sorghum bicolor</i> (L.). Plant Gene, 2015, 1, 18-28.	1.4	65
107	In silico characterization and expression analysis of selected Arabidopsis receptor-like kinase genes responsive to different MAMP inducers. Biologia Plantarum, 2015, 59, 18-28.	1.9	11
108	Two Promoters of Beta-Glucosidase Paralogs (<i>ZmBGLu2</i> and <i>ZmBGLu5</i>) Highly Active in Tropical Young Maize Hybrid Seedlings. Plant Molecular Biology Reporter, 2015, 33, 1666-1674.	1.0	2

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109	Homotypic clustering of OsMYB4 binding site motifs in promoters of the rice genome and cellular-level implications on sheath blight disease resistance. <i>Gene</i> , 2015, 561, 209-218.	1.0	16
110	Identification of genes induced by <i>Fusarium graminearum</i> inoculation in the resistant durum wheat line Langdon(Dic-3A)10 and the susceptible parental line Langdon. <i>Microbiological Research</i> , 2015, 177, 53-66.	2.5	7
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113	Genome-wide analysis reveals phytohormone action during cassava storage root initiation. <i>Plant Molecular Biology</i> , 2015, 88, 531-543.	2.0	46
114	Involvement of the Putative N-Acetylornithine Deacetylase from <i>Arabidopsis thaliana</i> in Flowering and Fruit Development. <i>Plant and Cell Physiology</i> , 2015, 56, 1084-1096.	1.5	45
115	Multiple tissue-specific expression of rice seed-shattering gene SH4 regulated by its promoter pSH4. <i>Rice</i> , 2015, 8, 12.	1.7	15
116	Identification and Mode of Inheritance of Quantitative Trait Loci for Secondary Metabolite Abundance in Tomato. <i>Plant Cell</i> , 2015, 27, 485-512.	3.1	188
117	Isolation and characterization of three cadmium-inducible promoters from <i>Oryza sativa</i> . <i>Journal of Biotechnology</i> , 2015, 216, 11-19.	1.9	13
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121	The complete peach dehydrin family: characterization of three recently recognized genes. <i>Tree Genetics and Genomes</i> , 2015, 11, 1.	0.6	7
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124	Basic Leucine Zipper Family in Barley: Genome-Wide Characterization of Members and Expression Analysis. <i>Molecular Biotechnology</i> , 2015, 57, 12-26.	1.3	75
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126	CicerTransDB 1.0: a resource for expression and functional study of chickpea transcription factors. <i>BMC Plant Biology</i> , 2016, 16, 169.	1.6	16

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128	The homeodomain transcription factor Ta HDZ1 from wheat regulates frost tolerance, flowering time and spike development in transgenic barley. <i>New Phytologist</i> , 2016, 211, 671-687.	3.5	26
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135	PlantPAN 2.0: an update of plant promoter analysis navigator for reconstructing transcriptional regulatory networks in plants. <i>Nucleic Acids Research</i> , 2016, 44, D1154-D1160.	6.5	336
136	Analysis of cis-acting regulatory elements of Respiratory burst oxidase homolog (Rboh) gene families in Arabidopsis and rice provides clues for their diverse functions. <i>Computational Biology and Chemistry</i> , 2016, 62, 104-118.	1.1	65
137	Identification and bioinformatics comparison of two novel phosphatases in monoecious and gynoeccious cucumber lines. <i>Proceedings of SPIE</i> , 2016, , .	0.8	4
138	Diverse responses of wild and cultivated tomato to BABA, oligandrin and <i>Oidium neolycopersici</i> infection. <i>Annals of Botany</i> , 2017, 119, mcw188.	1.4	11
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